

SEQUENCE LISTING

<110> Thompson, John E.
Wang, Tzann-Wei
Hudak, Katalin
Hong, Yuwen

<120> DNA ENCODING A PLANT LIPASE, TRANSGENIC PLANTS AND A
METHOD FOR CONTROLLING SENESCENCE IN PLANTS

<130> 10799/8

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<150> 09/250,280

<151> 1999-02-16

<150> 09/105,812

<151> 1998-06-26

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 1537

<212> DNA

<213> *Dianthus caryophyllus*

<400> 1

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 35 40 45
 Gln Val Thr Tyr Asp Thr Phe Ile Asn Asp Gln Asn Ser Ser Tyr Cys
 50 55 60
 Gly Ser Ser Arg Tyr Glu Lys Ala Asp Leu Leu His Lys Thr Ala Phe
 65 70 75 80
 Pro Gly Gly Ala Asp Arg Phe Asp Val Val Ala Tyr Leu Tyr Ala Thr
 85 90 95
 Ala Lys Val Ser Val Pro Glu Ala Phe Leu Leu Lys Ser Arg Ser Arg
 100 105 110
 Glu Lys Trp Asp Arg Glu Ser Asn Trp Ile Gly Tyr Val Val Val Ser
 115 120 125
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 130 135 140
 Trp Arg Gly Thr Cys Arg Asp Tyr Glu Trp Val Asp Val Leu Gly Ala
 145 150 155 160
 Gln Leu Glu Ser Ala His Pro Leu Leu Arg Thr Gln Gln Thr Thr His
 165 170 175
 Val Glu Lys Val Glu Asn Glu Glu Lys Lys Ser Ile His Lys Ser Ser
 180 185 190
 Trp Tyr Asp Cys Phe Asn Ile Asn Leu Leu Gly Ser Ala Ser Lys Asp
 195 200 205
 Lys Gly Lys Gly Ser Asp Asp Asp Asp Asp Asp Asp Pro Lys Val Met
 210 215 220
 Gln Gly Trp Met Thr Ile Tyr Thr Ser Glu Asp Pro Lys Ser Pro Phe
 225 230 235 240
 Thr Lys Leu Ser Ala Arg Thr Gln Leu Gln Thr Lys Leu Lys Gln Leu
 245 250 255
 Met Thr Lys Tyr Lys Asp Glu Thr Leu Ser Ile Thr Phe Ala Gly His
 260 265 270

Ser Leu Gly Ala Thr Leu Ser Val Val Ser Ala Phe Asp Ile Val Glu
 275 280 285
 Asn Leu Thr Thr Glu Ile Pro Val Thr Ala Val Val Phe Gly Cys Pro
 290 295 300
 Lys Val Gly Asn Lys Lys Phe Gln Gln Leu Phe Asp Ser Tyr Pro Asn
 305 310 315 320
 Leu Asn Val Leu His Val Arg Asn Val Ile Asp Leu Ile Pro Leu Tyr
 325 330 335
 Pro Val Lys Leu Met Gly Tyr Val Asn Ile Gly Ile Glu Leu Glu Ile
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 Asp Ser Arg Lys Ser Thr Phe Leu Lys Asp Ser Lys Asn Pro Ser Asp
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 Trp His Asn Leu Gln Ala Ile Leu His Val Val Ser Gly Trp His Gly
 370 375 380
 Val Lys Gly Glu Phe Lys Val Val Asn Lys Arg Ser Val Ala Leu Val
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 <213> Lycopersicon esculentum

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 <212> PRT
 <213> Dianthus caryophyllus

<400> 4
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 1 5 10

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Ala Asp Ser Leu Leu His Pro Lys Ser Leu Gln Lys Gly Ile Asn Asn
15 20 25 30

aag aac gat gag gat gag gac gag gac gag gat gag atc aaa gta atg 143
Lys Asn Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Ile Lys Val Met
35 40 45

gat ggg tgg ctt aag atc tac gtc tca agt aac ccg aag tcg tct ttc 191
Asp Gly Trp Leu Lys Ile Tyr Val Ser Ser Asn Pro Lys Ser Ser Phe
50 55 60

acg aga cta agt gca aga gaa caa ctt caa gca aag att gaa aag tta 239
Thr Arg Leu Ser Ala Arg Glu Gln Leu Gln Ala Lys Ile Glu Lys Leu
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aga aat gag tat aaa gat gag aat ttg agc ata act ttt aca ggg cat 287
Arg Asn Glu Tyr Lys Asp Glu Asn Leu Ser Ile Thr Phe Thr Gly His
80 85 90

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Ser Leu Gly Ala Ser Leu Ala Val Leu Ala Ser Phe Asp Val Val Glu
95 100 105 110

aat ggt gtg cca gtt gat att cca gta tct gca att gta ttt ggt agt 383
Asn Gly Val Pro Val Asp Ile Pro Val Ser Ala Ile Val Phe Gly Ser
115 120 125

cca caa gtt ggg aat aag gca ttc aat gaa aga atc aag aaa ttc tca 431
Pro Gln Val Gly Asn Lys Ala Phe Asn Glu Arg Ile Lys Lys Phe Ser
130 135 140

aac ttg aat atc tta cat gtt aag aac aag att gat ctc att acc ctt 479
Asn Leu Asn Ile Leu His Val Lys Asn Lys Ile Asp Leu Ile Thr Leu
145 150 155

tac cca agt gct ctg ttt ggg tat gtg aat tca g gtattgaagg 523
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→ ^{Ca} protection Seq. data missing (for above seq.)

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<213> Arabidopsis sp.

<400> 9

<400> 9
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<210> 11
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 <212> PRT
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 35 40 45
 Gln Val Thr Tyr Asp Thr Phe Ile Asn Asp Gln Asn Ser Ser Tyr Cys
 50 55 60
 Gly Ser Ser Arg Tyr Gly Lys Ala Asp Leu Leu His Lys Thr Ala Phe
 65 70 75 80
 Pro Gly Gly Ala Asp Arg Phe Asp Val Val Ala Tyr Leu Tyr Ala Thr
 85 90 95
 Ala Lys Val Ser Val Pro Glu Ala Phe Leu Leu Lys Ser Arg Ser Arg
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 Glu Lys Trp Asp Arg Glu Ser Asn Trp Ile Gly Tyr Val Val Val Ser
 115 120 125
 Asn Asp Glu Thr Ser Arg Val Ala Gly Arg Arg Glu Val Tyr Val Val
 130 135 140
 Trp Arg Gly Thr Cys Arg Asp Tyr Glu Trp Val Asp Val Leu Gly Ala
 145 150 155 160
 Gln Leu Glu Ser Ala His Pro Leu Leu Arg Thr Gln Gln Thr Thr His
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 Val Glu Lys Val Glu Asn Glu Glu Lys Lys Ser Ile His Lys Ser Ser
 180 185 190
 Trp Tyr Asp Cys Phe Asn Ile Asn Leu Leu Gly Ser Ala Ser Lys Asp
 195 200 205
 Lys Gly Lys Gly Ser Asp Asp Asp Asp Asp Asp Pro Lys Val Met
 210 215 220
 Gln Gly Trp Met Thr Ile Tyr Thr Ser Glu Asp Pro Lys Ser Pro Phe
 225 230 235 240

Thr Lys Leu Ser Ala Arg Thr Gln Leu Gln Thr Lys Leu Lys Cys Leu
 245 250 255
 Met Thr Lys Tyr Lys Asp Glu Thr Leu Ser Ile Thr Phe Ala Gly His
 260 265 270
 Ser Leu Gly Ala Thr Leu Ser Val Val Ser Ala Phe Asp Ile Val Glu
 275 280 285
 Asn Leu Thr Thr Glu Ile Pro Val Thr Ala Val Val Phe Gly Cys Pro
 290 295 300
 Lys Val Gly Asn Lys Lys Phe Gln Gln Leu Phe Asp Ser Tyr Pro Asn
 305 310 315 320
 Leu Asn Val Leu His Val Arg Asn Val Ile Asp Leu Ile Pro Leu Tyr
 325 330 335
 Pro Val Lys Leu Met Gly Tyr Val Asn Ile Gly Ile Glu Leu Glu Ile
 340 345 350
 Asp Ser Arg Lys Ser Thr Phe Leu Lys Asp Ser Lys Asn Pro Ser Asp
 355 360 365
 Trp His Asn Leu Gln Ala Ile Leu His Val Val Ser Gly Trp His Gly
 370 375 380
 Val Lys Gly Glu Phe Lys Val Val Asn Lys Arg Ser Val Ala Leu Val
 385 390 395 400
 Asn Lys Ser Cys Asp Phe Leu Lys Glu Glu Cys Leu Val Pro Pro Ala
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 420 425 430
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 35 40 45
 His Tyr Gly Glu Met Ala Gln Ala Gly Tyr Asp Thr Phe Asn Ile Asn
 50 55 60

Thr Glu Ser Gln Phe Ala Gly Ala Ser Ile Tyr Ser Arg Lys Asp Phe
 65 70 75 80
 Phe Ala Lys Val Gly Leu Glu Ile Ala His Pro Tyr Thr Lys Tyr Lys
 85 90 95
 Val Thr Lys Phe Ile Tyr Ala Thr Ser Asp Ile His Val Pro Glu Ser
 100 105 110
 Phe Leu Leu Phe Pro Ile Ser Arg Glu Gly Trp Ser Lys Glu Ser Asn
 115 120 125
 Trp Met Gly Tyr Val Ala Val Thr Asp Asp Gln Gly Thr Ala Leu Leu
 130 135 140
 Gly Arg Arg Asp Ile Val Val Ser Trp Arg Gly Ser Val Gln Pro Leu
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 Glu Trp Val Glu Asp Phe Glu Phe Gly Leu Val Asn Ala Ile Lys Ile
 165 170 175
 Phe Gly Glu Arg Asn Asp Gln Val Gln Ile His Gln Gly Trp Tyr Ser
 180 185 190
 Ile Tyr Met Ser Gln Asp Glu Arg Ser Pro Phe Thr Lys Thr Asn Ala
 195 200 205
 Arg Asp Gln Val Leu Arg Glu Val Gly Arg Leu Leu Glu Lys Tyr Lys
 210 215 220
 Asp Glu Glu Val Ser Ile Thr Ile Cys Gly His Ser Leu Gly Ala Ala
 225 230 235 240
 Leu Ala Thr Asp Ser Ala Ile Asp Ile Val Ala Asn Gly Tyr Asn Arg
 245 250 255
 Pro Lys Ser Arg Pro Asp Lys Ser Cys Pro Val Thr Ala Phe Val Phe
 260 265 270
 Ala Ser Pro Arg Val Gly Asp Ser Asp Phe Arg Lys Leu Phe Ser Gly
 275 280 285
 Leu Glu Asp Ile Arg Val Leu Arg Thr Arg Asn Leu Phe Asp Val Ile
 290 295 300
 Pro Ile Tyr Pro Pro Ile Gly Tyr Ser Glu Val Gly Asp Glu Phe Pro
 305 310 315 320
 Ile Asp Thr Arg Lys Ser Pro Tyr Met Lys Ser Pro Gly Asn Leu Ala
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 Thr Phe His Cys Leu Glu Gly Tyr Leu His Gly Val Ala Gly Thr Gln
 340 345 350
 Gly Thr Asn Lys Ala Asp Leu Phe Arg Leu Asp Val Glu Arg Ala Ile
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Gly Leu Val Asn Lys Ser Val Asp Gly Leu Lys Asp Glu Cys Met Val
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Asp Phe

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<212> PRT
<213> Ipomoea sp.

<400> 13
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35 40 45

Glu Ala Ala Ser Lys Asn Val Gly Leu Pro Arg Tyr Ala Arg Arg Asn
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Leu Leu Ala Asn Cys Gly Leu Val Lys Gly Asn Pro Phe Lys Tyr Glu
65 70 75 80

Val Thr Lys Tyr Phe Tyr Ala Pro Ser Thr Ile Pro Leu Pro Asp Glu
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Gly Tyr Asn Val Arg Ala Thr Arg Ala Asp Ala Val Leu Lys Glu Ser
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Asn Trp Asn Gly Tyr Val Ala Val Ala Thr Asp Glu Gly Lys Val Ala
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Leu Gly Arg Arg Asp Ile Leu Ile Val Trp Arg Gly Thr Ile Arg Lys
130 135 140

Ser Glu Trp Asn Glu Asn Leu Thr Phe Trp Phe Val Lys Ala Pro Leu
145 150 155 160

Phe Phe Gly Gln Asn Ser Asp Pro Leu Val His Lys Gly Trp Tyr Asp
165 170 175

Met Tyr Thr Thr Ile Asn Gln Asp Ser Gln Leu Asn Glu Lys Ser Ala
180 185 190

Arg Asp Gln Ile Arg Glu Glu Val Ala Arg Leu Val Glu Leu Tyr Lys
195 200 205

Asp Glu Asp Ile Ser Ile Thr Val Thr Gly His Ser Leu Gly Ser Ser
 210 215 220
 Met Ala Thr Leu Asn Ala Val Asp Leu Ala Ala Asn Pro Ile Asn Asn
 225 230 235 240
 Asn Lys Asn Ile Leu Val Thr Ala Phe Leu Tyr Ala Ser Pro Lys Val
 245 250 255
 Gly Asp Glu Asn Phe Lys Asn Val Ile Ser Asn Gln Gln Asn Leu Arg
 260 265 270
 Ala Leu Arg Ile Ser Asp Val Asn Asp Ile Val Thr Ala Val Pro Pro
 275 280 285
 Phe Gly Trp Lys Glu Cys Asp Asn Thr Ala Ile Leu Tyr Gly Asp Val
 290 295 300
 Gly Val Gly Leu Val Ile Asp Ser Lys Lys Ser His Tyr Leu Lys Pro
 305 310 315 320
 Asp Phe Pro Asn Leu Ser Thr His Asp Leu Met Leu Tyr Met His Ala
 325 330 335
 Ile Asp Gly Tyr Gln Gly Ser Gln Gly Gly Phe Glu Arg Gln Glu Asp
 340 345 350
 Phe Asp Leu Ala Lys Val Asn Lys Tyr Gly Asp Tyr Leu Lys Ala Glu
 355 360 365
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 35 40 45
 Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp
 50 55 60

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Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe
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Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr
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Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser
100 105 110

Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val
115 120 125

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145 150 155 160

Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys
165 170 175

Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr
180 185 190

Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln
195 200 205

Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp
210 215 220

Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala
225 230 235 240

Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg
245 250 255

Ser Lys Lys Gly Lys Val Ile Pro Val Thr Ala Val Leu Thr Tyr Gly
260 265 270

Gly Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu
275 280 285

Gly Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys
290 295 300

Ser Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys
305 310 315 320

Ile Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu
325 330 335

Ala Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val
340 345 350

Ser Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr
355 360 365

His Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala
 370 375 380

Leu Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro
 385 390 395 400

Pro Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu
 405 410 415

Gly Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser
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 435 440 445

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<212> DNA

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 Asn Phe Leu Tyr Ala Thr Ala Arg Val Ser Leu Pro Glu Gly Leu Leu
 20 25 30

ctc caa tca caa tca aga gat tct tgg gac cgt gag tct aac tgg ttt 144
 Leu Gln Ser Gln Ser Arg Asp Ser Trp Asp Arg Glu Ser Asn Trp Phe
 35 40 45

ggc tac att gct gtc acg tct gat gaa cgg tct aag gct tta gga cgc 192
 Gly Tyr Ile Ala Val Thr Ser Asp Glu Arg Ser Lys Ala Leu Gly Arg
 50 55 60

cgt gag atc tat ata gct ttg aga gga acg agc agg aac tat gag tgg 240
 Arg Glu Ile Tyr Ile Ala Leu Arg Gly Thr Ser Arg Asn Tyr Glu Trp
 65 70 75 80

gtc aat gtt ttg ggt gct agg cca act tca gct gac ccc ttg ctg cac 288
 Val Asn Val Leu Gly Ala Arg Pro Thr Ser Ala Asp Pro Leu Leu His
 85 90 95

gga ccc gag cag gat ggt tct ggt ggt gta gtt gaa ggt acg act ttt 336
 Gly Pro Glu Gln Asp Gly Ser Gly Gly Val Val Glu Gly Thr Thr Phe
 100 105 110

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 115 120 125

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 130 135 140

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 Ser Leu Arg Ser Gln Leu Leu Ala Lys Ile Lys Glu Leu Leu Leu Lys
 145 150 155 160

tat aag gac gag aaa ccg agc att gtg ttg act gga cat agc ttg gga 528
 Tyr Lys Asp Glu Lys Pro Ser Ile Val Leu Thr Gly His Ser Leu Gly
 165 170 175

cct aca gag gct gtt ctg gcc gcc tat gat ata gct gag aac ggt tcc 576
 Pro Thr Glu Ala Val Leu Ala Ala Tyr Asp Ile Ala Glu Asn Gly Ser
 180 185 190

agt gat gat gtt ccg gtc act gct ata gtc ttt ggt tgt cca cag gta 624
 Ser Asp Asp Val Pro Val Thr Ala Ile Val Phe Gly Cys Pro Gln Val
 195 200 205

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 Gly Asn Lys Glu Phe Arg Asp Glu Val Met Ser His Lys Asn Leu Lys
 210 215 220

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 Ile Leu His Val Arg Asn Thr Ile Asp Leu Leu Thr Arg Tyr Pro Gly
 225 230 235 240

gga ctt tta ggg tat gtg gac ata gga ata aac ttt gtg atc gat aca 768
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 245 250 255

aag aag tca ccg ttc cta agc gat tca agg aat cca ggg gat tgg cat 816
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 260 265 270

aat ctt cag gcg atg tta cat gtt gta gct gga tgg aat ggg aag aaa 864
 Asn Leu Gln Ala Met Leu His Val Val Ala Gly Trp Asn Gly Lys Lys
 275 280 285

gga gag ttt aaa ctg atg gtt aag aga agt att gca tta gtg aac aag 912
 Gly Glu Phe Lys Leu Met Val Lys Arg Ser Ile Ala Leu Val Asn Lys
 290 295 300

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 Ser Cys Glu Phe Leu Lys Ala Glu Cys Leu Val Pro Gly Ser Trp Trp
 305 310 315 320

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 Val Glu Lys Asn Lys Gly Leu Ile Lys Asn Glu Asp Gly Glu Trp Val
 325 330 335

ctt gct ccc gtt gaa gaa gaa cct gta cct gaa ttc taaattgtat 1054
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ttctgtattt ttctctaagg tcatgataaaa tcaacaataa gcagttcaac tatgtgatga 1114

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1167

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 <213> Arabidopsis sp.

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 Gly Tyr Ile Ala Val Thr Ser Asp Glu Arg Ser Lys Ala Leu Gly Arg
 50 55 60
 Arg Glu Ile Tyr Ile Ala Leu Arg Gly Thr Ser Arg Asn Tyr Glu Trp
 65 70 75 80
 Val Asn Val Leu Gly Ala Arg Pro Thr Ser Ala Asp Pro Leu Leu His
 85 90 95
 Gly Pro Glu Gln Asp Gly Ser Gly Gly Val Val Glu Gly Thr Thr Phe
 100 105 110
 Asp Ser Asp Ser Glu Asp Glu Glu Gly Cys Lys Val Met Leu Gly Trp
 115 120 125
 Leu Thr Ile Tyr Thr Ser Asn His Pro Glu Ser Lys Phe Thr Lys Leu
 130 135 140
 Ser Leu Arg Ser Gln Leu Leu Ala Lys Ile Lys Glu Leu Leu Leu Lys
 145 150 155 160
 Tyr Lys Asp Glu Lys Pro Ser Ile Val Leu Thr Gly His Ser Leu Gly
 165 170 175
 Pro Thr Glu Ala Val Leu Ala Ala Tyr Asp Ile Ala Glu Asn Gly Ser
 180 185 190
 Ser Asp Asp Val Pro Val Thr Ala Ile Val Phe Gly Cys Pro Gln Val
 195 200 205
 Gly Asn Lys Glu Phe Arg Asp Glu Val Met Ser His Lys Asn Leu Lys
 210 215 220
 Ile Leu His Val Arg Asn Thr Ile Asp Leu Leu Thr Arg Tyr Pro Gly
 225 230 235 240
 Gly Leu Leu Gly Tyr Val Asp Ile Gly Ile Asn Phe Val Ile Asp Thr
 245 250 255

Lys Lys Ser Pro Phe Leu Ser Asp Ser Arg Asn Pro Gly Asp Trp His
 260 265 270

Asn Leu Gln Ala Met Leu His Val Val Ala Gly Trp Asn Gly Lys Lys
 275 280 285

Gly Glu Phe Lys Leu Met Val Lys Arg Ser Ile Ala Leu Val Asn Lys
 290 295 300

Ser Cys Glu Phe Leu Lys Ala Glu Cys Leu Val Pro Gly Ser Trp Trp
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Val Glu Lys Asn Lys Gly Leu Ile Lys Asn Glu Asp Gly Glu Trp Val
 325 330 335

Leu Ala Pro Val Glu Glu Glu Pro Val Pro Glu Phe
 340 345

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<211> 195

<212> PRT

<213> Lycopersicon esculentum

<400> 17

Asp Tyr Glu Trp Val Asp Val Leu Gly Ala Arg Pro Asp Ser Ala Asp
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Ser Leu Leu His Pro Lys Ser Leu Gln Lys Gly Ile Asn Asn Lys Asn
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Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Ile Lys Val Met Asp Gly
 35 40 45

Trp Leu Lys Ile Tyr Val Ser Ser Asn Pro Lys Ser Ser Phe Thr Arg
 50 55 60

Leu Ser Ala Arg Glu Gln Leu Gln Ala Lys Ile Glu Lys Leu Arg Asn
 65 70 75 80

Glu Tyr Lys Asp Glu Asn Leu Ser Ile Thr Phe Thr Gly His Ser Leu
 85 90 95

Gly Ala Ser Leu Ala Val Leu Ala Ser Phe Asp Val Val Glu Asn Gly
 100 105 110

Val Pro Val Asp Ile Pro Val Ser Ala Ile Val Phe Gly Ser Pro Gln
 115 120 125

Val Gly Asn Lys Ala Phe Asn Glu Arg Ile Lys Lys Phe Ser Asn Leu
 130 135 140

Asn Ile Leu His Val Lys Asn Lys Ile Asp Leu Ile Thr Leu Tyr Pro
 145 150 155 160

Ser Ala Leu Phe Gly Tyr Val Asn Ser Gly Ile Glu Leu Val Ile Asp
 165 170 175

Ser Arg Lys Ser Pro Ser Leu Lys Asp Ser Lys Asp Met Gly Asp Trp
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His Asn Leu
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 aga aga cta aga gac acg tgg cgt aag atc caa gga gaa gac gat tgg 96
 Arg Arg Leu Arg Asp Thr Trp Arg Lys Ile Gln Gly Glu Asp Asp Trp
 20 25 30
 gcc ggg tta atg gat cca atg gat cca att ctt aga tcg gag cta atc 144
 Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile
 35 40 45
 cgt tac ggc gaa atg gct caa gct tgt tac gac gct ttc gat ttc gat 192
 Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp
 50 55 60
 ccc gct tcc aaa tac tgc ggc acc tcc agg ttc acg cga ctc gag ttc 240
 Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe
 65 70 75 80
 ttc gat tct ctc gga atg atc gat tcc ggt tac gag gtg gcg cgt tac 288
 Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr
 85 90 95
 ctc tac gcg acg tcg aac atc aat ctc ccg aac ttc ttc tcg aaa tcg 336
 Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser
 100 105 110
 cgg tgg tct aaa gtc tgg agc aaa aac gct aat tgg atg gga tac gtc 384
 Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val
 115 120 125
 gcc gtt tca gac gac gaa acg tct cgt aac cga ctc ggc cgc cgt gat 432
 Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp
 130 135 140
 atc gcg att gcg tgg aga gga acc gtt acg aaa ctt gaa tgg atc gcg 480
 Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala
 145 150 155 160

gat cta aag gat tat tta aaa ccg gta acc gaa aac aag atc cga tgc 528
 Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys
 165 170 175

ccc gac ccg gcc gtt aaa gtc gaa tcc gga ttc tta gat ctc tac act 576
 Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr
 180 185 190

gac aaa gac aca acc tgc aaa ttc gcg aga ttc tca gcg cgt gaa cag 624
 Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln
 195 200 205

att tta acg gag gtg aaa ccg tta gtg gaa gaa cac ggc gac gac gat 672
 Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp
 210 215 220

gat tcc gat tta agc atc acc gtg acg gga cac agt ctc ggc ggc gcg 720
 Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala
 225 230 235 240

tta gcg ata tta agc gcg tac gat ata gcg gag atg aga ttg aat ccg 768
 Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg
 245 250 255

agt aag aaa ggg aaa gtg att ccg gtg acg gtg ttg aca tac gga gga 816
 Ser Lys Lys Gly Lys Val Ile Pro Val Thr Val Leu Thr Tyr Gly Gly
 260 265 270

ccg aga gtt ggg aac gtt agg ttt agg gag agg atg gag gaa ttg gga 864
 Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu Gly
 275 280 285

gtg aaa gtg atg aga gta gtg aat gtt cac gac gtg gtt ccc aag tcg 912
 Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys Ser
 290 295 300

ccg gga ttg ttt ttg aac gag agt aga cct cac gcg ctg atg aag ata 960
 Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys Ile
 305 310 315 320

gcg gag ggg ttg ccg tgg tgt tat agc cac gtg ggg gag gag ctg gcg 1008
 Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu Ala
 325 330 335

ttg gat cat cag aac tcg ccg ttt ctt aaa cct tcc gtt gat gtt tct 1056
 Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val Ser
 340 345 350

act gct cat aat ctt gaa gct atg ctt cat tta ctt gac ggg tat cat 1104
 Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr His
 355 360 365

gga aaa gga gag aga ttt gtg ctg tcg agt ggg aga gac cat gcg cta 1152
 Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala Leu
 370 375 380

gtg aac aaa gcg tcg gac ttt ttg aaa gag cat tta caa att cca ccg 1200
 Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro Pro
 385 390 395 400

ttt tgg cgt caa gac gcg aat aaa gga atg gtt cgg aac agt gaa ggt 1248
 Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu Gly
 405 410 415

cgt tgg att caa gcc gag cgt ctc cgt ttt gag gat cat cat tct cct 1296
 Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser Pro
 420 425 430

gat atc cac cac cat ctc tct cag ctc cgt ctt gat cat cct tgt taa 1344
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Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile
 35 40 45

Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp
 50 55 60

Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe
 65 70 75 80

Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr
 85 90 95

Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser
 100 105 110

Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val
 115 120 125

Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp
 130 135 140

Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala
 145 150 155 160

Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys
 165 170 175

Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr
 180 185 190

Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln
 195 200 205
 Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp
 210 215 220
 Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala
 225 230 235 240
 Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg
 245 250 255
 Ser Lys Lys Gly Lys Val Ile Pro Val Thr Val Leu Thr Tyr Gly Gly
 260 265 270
 Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu Gly
 275 280 285
 Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys Ser
 290 295 300
 Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys Ile
 305 310 315 320
 Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu Ala
 325 330 335
 Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val Ser
 340 345 350
 Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr His
 355 360 365
 Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala Leu
 370 375 380
 Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro Pro
 385 390 395 400
 Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu Gly
 405 410 415
 Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser Pro
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 Asp Ile His His His Leu Ser Gln Leu Arg Leu Asp His Pro Cys
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<220>
<223> Description of Artificial Sequence: primer

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gatgagctcg acgaagctga gagagatg

28